

Abstract

A method for the detection of cytosine methylation in DNA samples is described, which is comprised of the following steps: First, a genomic DNA sample, which comprises the DNA to be investigated and background DNA, is chemically treated such that all unmethylated cytosine bases are converted to uracil, while the 5-methylcytosine bases remain unchanged. Then the chemically treated DNA sample is amplified with the use of at least 2 primer oligonucleotides as well as a polymerase, whereby the DNA to be investigated is preferred over the background DNA as the template, and in the last step, the amplicates are analyzed and the methylation status in the DNA to be investigated will be concluded from the presence of an amplicate and/or from the analysis of additional positions.